

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____

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Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
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Type of Search

NA Sequence (#) _____

AA Sequence (#) _____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems _____

WWW/Internet _____

Other (specify) _____



605
Delaval, Jan

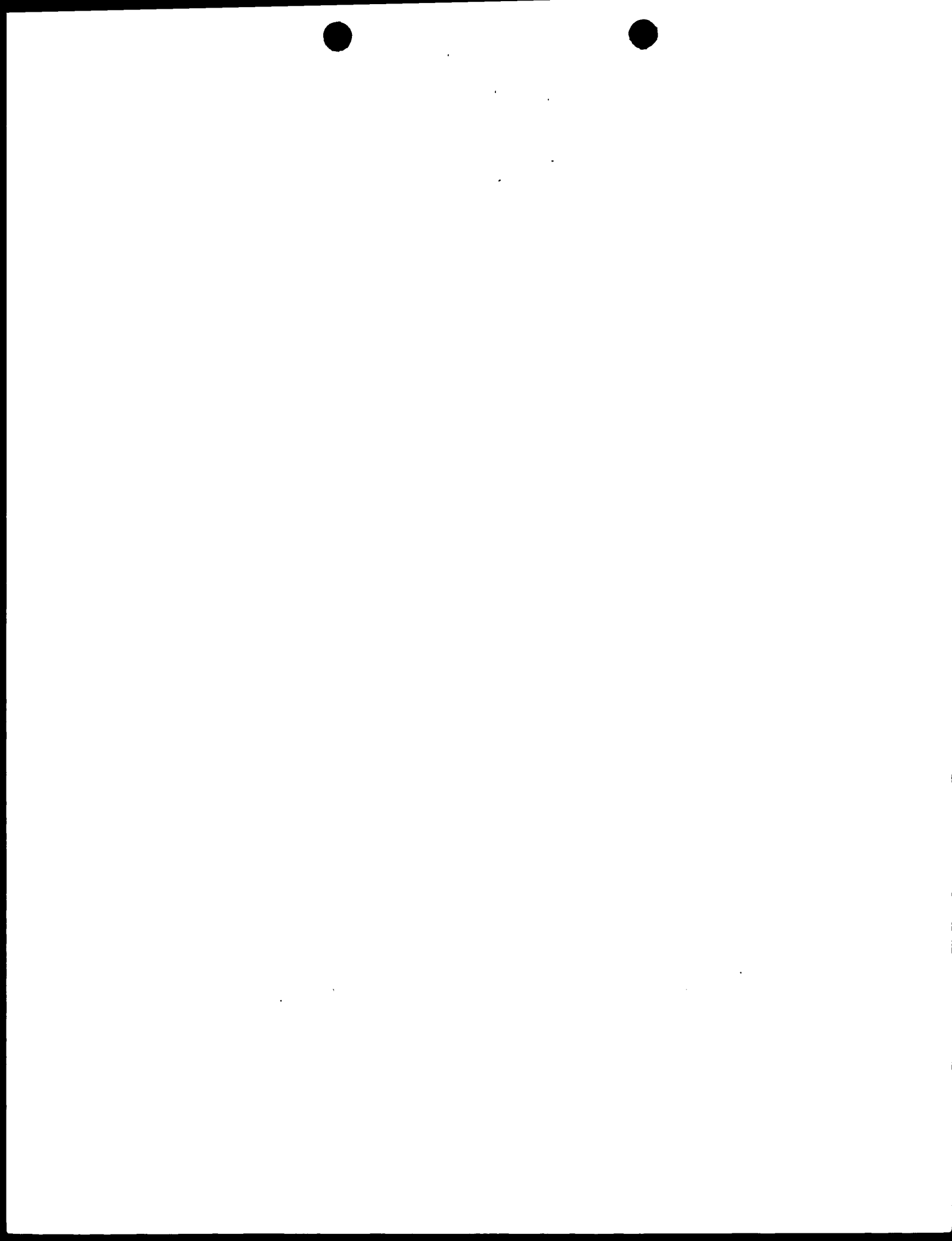
From: Jamroz, Margaret
Sent: Wednesday, February 13, 2002 10:27 AM
To: Delaval, Jan
Subject: 09/381,903

Jan,

Please do open search of SEQ ID NOS: 87, 88, 89, 90, 91, 92, and 93 of 09/381,903 with interference.

Thanks
Margaret (Megan) Jamroz
USPTO
AU 1644
Mailbox 9E12
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Jan Delaval
Reference Librarian
Biotechnology & Chemical Libr
CM1 1E07 - 703-308-4492
jan.delaval@uspto.gov



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08 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

09 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

10 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

11 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

12 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

13 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

14 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

15 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

16 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

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25 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

26 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

27 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

28 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

29 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

30 Protein: Protein search: 18. 2002. 18.28.29. 1. Search time: 12.59 seconds

28 107.5 8.4 98 2 US-07-814-220-2
29 107.5 8.4 98 2 US-07-814-220-2
30 107.5 8.4 98 2 US-07-814-220-2
31 106 8.3 742 2 US-08-105-175A-7
32 105.5 8.2 309 2 US-08-105-175A-7
33 104 8.1 219 2 US-08-105-175A-7
34 103.5 8.1 731 2 US-08-105-175A-7
35 103.5 8.1 731 2 US-08-105-175A-7
36 103.5 7.9 262 2 US-08-105-175A-7
37 101.5 7.9 263 2 US-08-105-175A-7
38 101.5 7.9 263 2 US-08-105-175A-7
39 101.5 7.9 263 2 US-08-105-175A-7
40 101.5 7.9 263 2 US-08-105-175A-7
41 100 7.8 1026 2 US-08-105-175A-7
42 100 7.8 1026 2 US-08-105-175A-7
43 100 7.8 1026 2 US-08-105-175A-7
44 99.5 7.8 805 4 US-08-105-175A-7
45 98.5 7.7 609 4 US-08-105-175A-7

ATTENTION

RESULT 1
US-08-440-861-2
Sequence 2, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
INVENTOR: Griffith, Irwin J.
TITLE OF INVENTION: A METHOD FOR THE PREPARATION OF POLYMERIZABLE
POLYMERIZABLE POLYMERIZABLE POLYMERIZABLE
ADDRESS: 60 State Street, Suite 500
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION NUMBER: US/08/440-861
APPLICATION DATE: 15-MAY-1995
CLASSIFICATION: A45
PRIORITY APPLICATION NUMBER: US/08/105-175A-7
FILING DATE: 15-MAY-1995
ATTORNEY/AGENCY: INFORMATION:
NAME: Amy E. Mandarinos
REGISTRATION NUMBER: 46,207
REFERENCE/INVENTOR INFORMATION:
TELEPHONE: (617) 227-5941
TELEFAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
POPULARITY: High
MOLECULE TYPE: Protein
US-08-440-861-2

Query Match: 77.6% Seq. No. 54, 18 11 Length 401
Best Local Similarity: 75.6% Seq. No. 40, 16 Indels 11 Gaps 5
Matches 208 Conservative 21 Missed Gaps 45

Protein No. is the number of results predicted by chance for a given score. No. is the number of results predicted by chance for a given score. No. is the number of results predicted by chance for a given score. No. is the number of results predicted by chance for a given score.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Protein
1	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
2	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
3	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
4	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
5	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
6	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
7	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
8	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
9	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
10	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
11	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
12	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
13	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
14	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
15	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
16	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
17	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
18	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
19	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
20	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
21	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
22	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
23	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
24	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
25	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
26	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl
27	993.5	77.6	401	US-08-440-861-2	Sequence 2, Appl

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Genome version 4.5
 Cytoscape (c) 1993 - 2000 Compugen Ltd.

Search time: 14.28 sec

Search time: 14.28 sec
 (without alignment)
 1.227.128 Million total updates/sec

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Genetic version 4.5

Copyright (c) 1994-2000 CompuLink Ltd.

M-protein protein search using SW model

February 13, 2002, 13:37:41 : Search time 5.78 seconds
(without alignment)

1636.072 hits (9.9% of database)

Hit list

Protein source: 08-09-381-903-87

Accession: 1-265

Description: 1-265

Spot list table: 1-265

Score: 10.0, Gap: 0.5

Search: 17605 spots, 14627.429 residues

Total number of hits satisfying chosen parameters: 17605

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post processing: Minimum Match 0.8

Maximum Match 1.00

Listing first 45 summaries

Database:

1: SP_000001

2: SP_000002

3: SP_000003

4: SP_000004

5: SP_000005

6: SP_000006

7: SP_000007

8: SP_000008

9: SP_000009

10: SP_000010

11: SP_000011

12: SP_000012

13: SP_000013

14: SP_000014

15: SP_000015

16: SP_000016

17: SP_000017

18: SP_000018

19: SP_000019

20: SP_000020

21: SP_000021

22: SP_000022

23: SP_000023

24: SP_000024

25: SP_000025

26: SP_000026

27: SP_000027

28: SP_000028

29: SP_000029

30: SP_000030

Prod. No. is the number of results predicted by chance. The lower a score the greater the probability of the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match length	ID	Protein
1	1.271	265	090800	phleum prat
2	1.271	265	090800	phleum prat
3	1.271	265	090800	phleum prat
4	1.271	265	090800	phleum prat
5	1.271	265	090800	phleum prat
6	1.271	265	090800	phleum prat
7	1.271	265	090800	phleum prat
8	1.271	265	090800	phleum prat
9	1.271	265	090800	phleum prat
10	1.271	265	090800	phleum prat
11	1.271	265	090800	phleum prat
12	1.271	265	090800	phleum prat
13	1.271	265	090800	phleum prat
14	1.271	265	090800	phleum prat
15	1.271	265	090800	phleum prat
16	1.271	265	090800	phleum prat
17	1.271	265	090800	phleum prat
18	1.271	265	090800	phleum prat
19	1.271	265	090800	phleum prat

20	545.5	42.6	31.3	10	004826	004828 barium vol
21	545.5	41.9	179	10	039995	039995 barium vol
22	439.5	26.5	138	10	065863	065863 phleum prat
23	412	24.4	106	10	065863	065863 phleum prat
24	182	14.2	722	13	014084	014084 diosostich
25	170	13.3	1147	2	087848	087848 streptomy
26	168.5	13.2	734	5	098102	098102 quadrus chi
27	166.5	13.0	362	13	090400	090400 diosostich
28	163.5	12.8	650	9	090308	090308 streptomy
29	157	12.3	675	13	090604	090604 diosostich
30	155.5	12.1	645	5	091176	091176 streptomy
31	154	12.0	1158	2	005158	005158 streptomy
32	154	12.0	1156	2	007270	007270 streptomy
33	153	12.0	507	13	014076	014076 diosostich
34	152	11.7	714	5	098171	098171 streptomy
35	150	11.7	595	2	095680	095680 streptomy
36	148.5	11.6	1156	2	097585	097585 streptomy
37	145.5	11.4	2016	5	098177	098177 streptomy
38	143.5	11.2	298	2	052086	052086 streptomy
39	143.5	11.2	1229	5	090401	090401 diosostich
40	143	11.2	3469	5	090401	090401 diosostich
41	143	11.2	4502	5	090401	090401 diosostich
42	142	11.1	2178	2	098177	098177 streptomy
43	141.5	11.1	2178	2	098177	098177 streptomy
44	141	11.0	1940	2	091176	091176 streptomy
45	138	10.8	805	5	001576	001576 streptomy

ALIGNED

Result	ID	Score	Match length	ID	Protein
1	090800	1.271	265	090800	phleum prat
2	090800	1.271	265	090800	phleum prat
3	090800	1.271	265	090800	phleum prat
4	090800	1.271	265	090800	phleum prat
5	090800	1.271	265	090800	phleum prat
6	090800	1.271	265	090800	phleum prat
7	090800	1.271	265	090800	phleum prat
8	090800	1.271	265	090800	phleum prat
9	090800	1.271	265	090800	phleum prat
10	090800	1.271	265	090800	phleum prat
11	090800	1.271	265	090800	phleum prat
12	090800	1.271	265	090800	phleum prat
13	090800	1.271	265	090800	phleum prat
14	090800	1.271	265	090800	phleum prat
15	090800	1.271	265	090800	phleum prat
16	090800	1.271	265	090800	phleum prat
17	090800	1.271	265	090800	phleum prat
18	090800	1.271	265	090800	phleum prat
19	090800	1.271	265	090800	phleum prat
20	090800	1.271	265	090800	phleum prat

Query Match: 99.4%, Score: 1.271, ID: 10, Length: 265, best local similarity: 99.2%, prod. No.: 1, 40, 74, matches: 265, conservative: 0, mismatches: 2, indels: 0, gaps: 0.

Accuracy Match	76.28%	Score	972.65	108.11	Length	301
Nearest Local Similarity	74.58%	Find. No.	4	36	Index	11
Articles	205	Conservative	22	Mismatches	37	

[illegible][illegible]

Database version 4.5
 Copyright (c) 1994 - 2000 Compugen Ltd.

on protein: protein search using sw model

Run on: February 13, 2002, 10:43:50 Search time 99.5 seconds
 (without alignments)
 493,125 Million cell updates/sec

Hit list:
 Post score: 1.27
 1 AAWARAT1AAA2AA3KA11AAWASAA1AAVAA1KVV 265

Sequence: HGGMM2
 Gap: 10.0, Gap: 0.5

Score table: 47405 seqs, 14627429 residues

Scored: 47405 seqs, 14627429 residues 47405

Total number of hits satisfying chosen parameters:
 Minimum 18 seq length: 0
 Maximum 18 seq length: 20000000

Post processing: Minimum Match 08
 Maximum Match 1000
 Listed first 45 summaries

Database: 1: SP_ARMED_17;
 2: SP_ARMED_17;
 3: SP_ARMED_17;
 4: SP_ARMED_17;
 5: SP_ARMED_17;
 6: SP_ARMED_17;
 7: SP_ARMED_17;
 8: SP_ARMED_17;
 9: SP_ARMED_17;
 10: SP_ARMED_17;
 11: SP_ARMED_17;
 12: SP_ARMED_17;
 13: SP_ARMED_17;
 14: SP_ARMED_17;

Prod. No. is the number of results predicted by chance for a given score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length DB	ID	Description
1	1250	97.9	265	10	Q9SBE0
2	1250	97.9	265	10	Q9SBE0
3	1242	97.3	261	10	Q9SBE0
4	1222	96.0	260	10	Q9SBE0
5	1185	95.4	287	10	Q9SBE0
6	1079	93.8	296	10	Q9SBE0
7	1014.5	92.4	303	10	Q9SBE0
8	972.5	90.4	301	10	Q9SBE0
9	962.5	89.4	301	10	Q9SBE0
10	940.5	87.3	312	10	Q9SBE0
11	840.5	85.8	276	10	Q9SBE0
12	838.5	85.5	276	10	Q9SBE0
13	837	85.5	276	10	Q9SBE0
14	824.5	84.6	276	10	Q9SBE0
15	824.5	84.6	276	10	Q9SBE0
16	810.5	83.8	240	10	Q9SBE0
17	810.5	83.8	240	10	Q9SBE0
18	810.5	83.8	240	10	Q9SBE0
19	696.5	84.5	276	10	Q9SBE0

20	546.5	42.8	314	10	Q9SBE0
21	536.5	42.0	179	10	Q9SBE0
22	318.5	24.9	138	10	Q9SBE0
23	291	22.8	106	10	Q9SBE0
24	183	14.3	722	13	Q9SBE0
25	173	14.5	1147	2	Q9SBE0
26	172.5	14.5	462	13	Q9SBE0
27	172.5	14.5	744	13	Q9SBE0
28	161.5	12.6	540	9	Q9SBE0
29	159	12.5	507	13	Q9SBE0
30	159	12.5	675	13	Q9SBE0
31	150.5	11.7	595	2	Q9SBE0
32	150	11.7	1158	2	Q9SBE0
33	150	11.7	1556	2	Q9SBE0
34	150	11.7	1845	5	Q9SBE0
35	146.5	11.5	2016	5	Q9SBE0
36	145.5	11.4	298	2	Q9SBE0
37	144.5	11.3	3409	5	Q9SBE0
38	144	11.3	3502	5	Q9SBE0
39	144	11.3	3409	5	Q9SBE0
40	142.5	11.2	2178	2	Q9SBE0
41	142	11.1	926	5	Q9SBE0
42	142	11.1	2639	5	Q9SBE0
43	140	11.0	1156	2	Q9SBE0
44	139	10.9	1514	5	Q9SBE0
45	137.5	10.8	1229	5	Q9SBE0

ALIGMENTS

Result	ID	Q9SBE0	PRELIMINARY:	Prod. No.	AA
1	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
2	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
3	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
4	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
5	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
6	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
7	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
8	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
9	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
10	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
11	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
12	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
13	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
14	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
15	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
16	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
17	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
18	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
19	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
20	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
21	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
22	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
23	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
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25	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
26	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
27	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
28	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
29	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
30	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
31	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
32	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
33	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
34	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
35	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
36	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
37	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
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40	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
41	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
42	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
43	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
44	Q9SBE0	Q9SBE0	Q9SBE0	265	AA
45	Q9SBE0	Q9SBE0	Q9SBE0	265	AA

Query Match: 97.98; Score: 1250; DB: 10; Length: 265;
 Prod. No. 2: 50-71;
 Matches: 260; Conservative: 1; P-values: 0; Gaps: 0;

[illegible][illegible]

February 18, 2002, 10:58:56 ; Search time 8.772 seconds
(withouthelp@redhat.com) (withouthelp@redhat.com)

Sequence	Length	Frequency
AAAAA	5	0.0001
AAAA	4	0.0001
AAA	3	0.0001
AA	2	0.0001
A	1	0.0001

See also: 0.5

10005+3035, 26664827 residuals

Maximum DB Set Length: 2000000000

Post-Processing:	Minimum	0%
	Maximum	100%
Listing	First 45	summaries

10412456 : 2W155101-99:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SILIMAKI 1:55

Protein No.	Score	Category	Length	100	110
1	1264	99.0	284	1	MP8R_PPIPR
2	966.5	67.1	333	1	MP92_PPIPR
3	843.5	67.1	373	1	MP91_PPIPR
4	842	65.7	307	1	MP94_PPIPR
5	826.5	64.7	266	1	MP9A_PPIPR
6	762.5	59.7	339	1	MP9C_PPIPR
7	706	56.3	320	1	MP9E_PPIPR
8	698	54.7	291	1	MP5E_PPIPR
9	619.5	45.4	175	1	MP4A_PPIPR
10	549.5	45.0	308	1	MP5A_PPIPR
11	483	45.8	305	1	MP5E_PPIPR
12	327.5	35.5	132	1	MP6E_PPIPR
13	136	14.4	760	1	AMP_NORIO
14	157	11.8	1561	1	SPAP_S1PR0
15	150	11.7	1565	1	PAC_STR00
16	145	11.7	1565	1	ALMT_STR0E
17	140.5	11.3	452	1	ALMT_STR0E
18	138.5	11.3	421	1	STRK_STR01
19	135	9.8	1120	1	ALMT_STR01
20	123.5	9.7	915	1	ALMT_STR01
21	121	9.5	901	1	ALMT_STR01
22	117.5	9.2	299	1	ALMT_STR01
23	115.5	9.0	662	1	ALMT_STR01
24	114	8.8	370	1	ALMT_STR01
25	112.5	8.6	450	1	ALMT_STR01
26	112	8.4	740	1	ALMT_STR01
27	110	8.4	744	1	ALMT_STR01
28	109	8.5	1025	1	ALMT_STR01
29	109	8.5	331	1	ALMT_STR01
30	108	8.5	762	1	ALMT_STR01
31	108	8.5	251	1	ALMT_STR01
32	108	8.5	453	1	ALMT_STR01
33	107	8.5	4838	1	ALMT_STR01
34	107	8.4	221	1	ALMT_STR01
					HC2X_CHLIR

34	106.5	8.3	240	1	HL2-V47A	CG0865, volutin coat
35	106	8.3	1083	1	T2B3-1A5N	CG0865, homo sapiens
36	105	8.2	361	1	P1R3-1A5N	CG4160 saccharomyces
37	105	8.2	530	1	Y49A-2C000	CG1080 scith. osobacter
38	105	8.2	640	1	Y051-2C0710	CG1080 mycobacter
39	105	8.2	1199	1	N121-1A71	CG5410 fume sapro- phytic
40	105	8.2	1348	1	1K82-1BMAN	P24645 mus. musculus
41	104.5	8.2	304	1	MA5S-1B05SC	CG11042 mycobacter
42	104.5	8.2	307	1	MC7E-1A7XX	CG11042 mycobacter
43	104	8.2	875	1	Y77A-1B711A	P29746 drosophila
44	104	8.1	442	1	BNH-1B0-ME	CG2410 drosophila
45	104	8.1	865	1	CPN-1C09DE	

ALUMINUM

[illegible]

FEBS Lett. 363:6-12(1995).

$$\mathbb{R}^N \quad (2)$$
REVISED
DATE:

Submitted (Sept. 1997) to the EMBO/CellPress/JMB Press

CC-1 - FUNCTION: HAS KIBRONOLAZONE IN THE
 PATENTED INTERACTIONS.

POLEON ALLERGY.
-1- DISTASTE FOR GRASS
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-100- DISTASTE FOR GRASS

1 - SIMILARITY: BELONGS TO THE SAME CATEGORY

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or send an email to info@openstax.org

PMID: 227083; CAA81609.1;

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Interpro; lpr002914; polleh_ali_14
Interpro; lpr002914; polleh_ali_14
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DR
HAM; PFO16Z0; POLIEN_4...
STUDY | A] Jergel.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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Pt	SIGNAL	<1	19	PERCENTAGE
28A		10	28A	PERCENT ALBUMIN PH. 1.56.

CHAIN	20	20
PT	284 AA	28001 MW
CO	284 AA	1994 PH 310985.295E. (K004)

99.08; SiO_2 1.64; H₂O 1.64; CaO 2.84;

Query matrix	Prod. No.	Model's	Caps
Post local similarity	99.28	0	0

Matches	Conservative	Mismatches
263	0	2

ADAGVAPATTPAAGGAAAKATTEETLEIIEINVGITKAVAASVIAALAFKIFEAATLS

[illegible]

20 AIDAGYAPATTPAAGAAAGKAI | EFGG | EIDLNVCH |

6.1 SSKAAAKA²(1,VPK1,5)AAVSVA²AAV(,ATP,AKT)SPVASLTHALRV[AG]A,1:VHAAR 120

[illegible]

1. The first part of the document is a list of references. The references are listed in a standard format, with the author's name, the title of the work, and the publisher. The references are as follows:

1. J. H. Van Veen, *The History of the Netherlands*, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578,

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Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 10⁸ cells/ml. The cells were then mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The asterisk indicates a significant difference (*p* < 0.05) between the two groups.

[illegible]

References

1 Sequence: 2, Appointed for US/0817474A
 2 Patent No.: 576,962
 3 GENERAL INFORMATION:
 4 APPLICANT: Smith, Melvin B.
 5 APPLICANT: Knox, Robert B.
 6 APPLICANT: Smith, Donald
 7 APPLICANT: Avjootian, Asil
 8 APPLICANT: Eberhardt, Fred
 9 APPLICANT: Eberhardt, Fred
 10 APPLICANT: Eberhardt, Fred
 11 APPLICANT: Eberhardt, Fred
 12 APPLICANT: Eberhardt, Fred
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 100 APPLICANT: Eberhardt, Fred

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GenBank version 4.5
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ORF protein - protein search using SW model

Run on: February 13, 2002, 10:44:44 : Search time 18.39 seconds
(without alignment)

112.774 Million cell updates/sec

Database: US-09-381-903-93

Protein source: NCBI/GenBank/GenBank

Protein length: 111

Scoring table:

Gap: 10.0 : gap: 0.5

Search: 21252 seqs, 2504292 residues

Number of hits satisfying chosen parameters: 21252

Minimum ORF seq length: 1

Maximum ORF seq length: 2000000

Post-processing: Minimum Match: 0K
Maximum Match: 100K
Listing first 45 summaries

Database: US-09-381-903-93

1: 76.0 100.0 100.0 100.0 100.0 100.0

2: 76.0 100.0 100.0 100.0 100.0 100.0

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Post. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ORF	ID	Description
1	883.5	76.0	401	1	US-08-440-861-2	Sequence 2, App1
2	883.5	76.0	401	1	US-08-440-861-2	Sequence 2, App1
3	883.5	76.0	401	1	US-08-174-745A-2	Sequence 2, App1
4	883.5	76.0	401	2	US-08-195-947-2	Sequence 2, App1
5	883.5	76.0	401	2	US-08-443-885-2	Sequence 2, App1
6	883.5	76.0	401	2	US-08-443-908-2	Sequence 2, App1
7	883.5	76.0	401	4	US-08-410-614-2	Sequence 2, App1
8	883.5	76.0	401	4	US-08-443-854-4	Sequence 4, App1
9	883.5	76.0	401	4	US-08-174-745A-4	Sequence 4, App1
10	883.5	76.0	401	2	US-08-195-947-2	Sequence 2, App1
11	883.5	76.0	401	2	US-08-443-885-2	Sequence 2, App1
12	883.5	76.0	401	2	US-08-443-908-2	Sequence 2, App1
13	883.5	76.0	401	4	US-08-410-614-2	Sequence 2, App1
14	883.5	76.0	401	4	US-08-443-854-4	Sequence 4, App1
15	883.5	76.0	401	4	US-08-174-745A-4	Sequence 4, App1
16	883.5	76.0	401	2	US-08-195-947-2	Sequence 2, App1
17	883.5	76.0	401	2	US-08-443-885-2	Sequence 2, App1
18	883.5	76.0	401	2	US-08-443-908-2	Sequence 2, App1
19	883.5	76.0	401	4	US-08-410-614-2	Sequence 2, App1
20	883.5	76.0	401	4	US-08-443-854-4	Sequence 4, App1
21	883.5	76.0	401	4	US-08-174-745A-4	Sequence 4, App1
22	883.5	76.0	401	2	US-08-195-947-2	Sequence 2, App1
23	883.5	76.0	401	2	US-08-443-885-2	Sequence 2, App1
24	883.5	76.0	401	2	US-08-443-908-2	Sequence 2, App1
25	883.5	76.0	401	4	US-08-410-614-2	Sequence 2, App1
26	883.5	76.0	401	4	US-08-443-854-4	Sequence 4, App1
27	883.5	76.0	401	4	US-08-174-745A-4	Sequence 4, App1

28	109.5	9.4	391	4	US-08-080-842-40	Sequence 40, App1
29	108.5	9.3	98	2	US-07-044-220-2	Sequence 2, App1
30	108.5	9.3	98	2	US-07-044-220-2	Sequence 2, App1
31	108	9.3	332	2	US-08-195-947-2	Sequence 2, App1
32	106	9.1	219	2	US-08-443-885-2	Sequence 2, App1
33	105.5	9.1	741	2	US-08-443-885-2	Sequence 2, App1
34	105.5	9.1	743	4	US-08-195-947-2	Sequence 4, App1
35	101.5	8.7	805	4	US-08-195-947-2	Sequence 4, App1
36	100.5	8.6	262	2	US-08-443-885-2	Sequence 2, App1
37	100.5	8.6	262	2	US-08-443-885-2	Sequence 2, App1
38	100.5	8.6	263	2	US-08-443-885-2	Sequence 2, App1
39	100.5	8.6	263	3	US-08-443-885-2	Sequence 3, App1
40	100.5	8.6	263	4	US-08-443-885-2	Sequence 4, App1
41	99.5	8.6	362	3	US-08-443-885-2	Sequence 3, App1
42	99.5	8.6	413	1	US-08-443-885-2	Sequence 1, App1
43	99.5	8.6	413	1	US-08-443-885-2	Sequence 1, App1
44	99.5	8.6	413	2	US-08-443-885-2	Sequence 2, App1
45	99.5	8.6	609	4	US-08-443-885-2	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-08-440-861-2 : Application US-08440861
Sequence 2, 5710126
Patient No. 5710126
GENERAL INFORMATION:
APPLICANT: GRIFFIN, Edwin J.
APPLICANT: Kuo, Mohamed
APPLICANT: Logman, Mohamed
TITLE OF INVENTION: 1. Amino acid sequence of a protein
NUMBER OF SEQUENCES: 56
ADDRESS: 60 State Street, Suite 110
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER BEAMABLE FORM:
MEDIUM TYPE: floppy disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/440-861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US-08/106-015
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandouras
REGISTRATION NUMBER: 36,207
REFERENCE/BOOKLET NUMBER: 1PC-015 (1M1-040-F2)
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-861-2

Query Match: 76.0% : Score: 883.5 : ORF: 1 : Length: 401:
Post Local Similarity: 69.5% : Pref No.: 1,50-78:
Matches: 191 : Conservative: 18 : Mismatches: 41 : Indels: 45 : Gaps: 4:

